

1600

RAW SEQUENCE LISTING DATE: 11/04/2003 PATENT APPLICATION: US/09/901,938A TIME: 10:01:50

Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\11032003\I901938A.raw

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3 <110> APPLICANT: ECONS, Michael WHITE, Kenneth STROM, Tim MEITINGER, Thomas
 W--> 4 <120> TITLE OF INVENTION: NOVEL FIBROBLAST GROWTH FACTOR (FGF23) AND METHODS FOR
  USE<130> 053884-
 W-- 5 <140> CURRENT APPLICATION NUMBER: 09/901,938A
                                                                         Does No Comply
       0 <130> FILE REFERENCE:
                                                                     Commerced to theme place of
      6 <141> CURRENT FILING DATE: 2001-07-10
        8 <150> PRIOR APPLICATION NUMBER: 60/219,137
insert 9 <151> prior filling date: 2000-07-19
 Wy-> 10 <160> NUMBER OF SEQ ID: 35 <170> Patentin version 3.0

W/d 13 <210> SEQ ID NO: 1

Lun 14 <211> LENGTH: 1612

Lunc 14 <211> LENGTH: 1612
                                                                   Corrected Dickette Needel
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       16 <213> ORGANISM: Homo sapiens
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       23 gcaccagcca ctcagagcag ggcacgatgt tgggggcccg cctcaggctc tgggtctgtg
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       25 cettgtgeag egtetgeage atgagegtee teagageeta teccaatgee tecceaetge
                                                                                  240
       27 teggetecag etggggtgge etgatecace tgtacacage cacagecagg aacagetace
                                                                                  300
                                                                                  360
       29 acctgcagat ccacaagaat ggccatgtgg atggcgcacc ccatcagacc atctacagtg
       31 ccctgatgat cagatcagag gatgctggct ttgtggtgat tacaggtgtg atgagcagaa
                                                                                  420
                                                                                  480
       33 gatacetetg catggattte agaggeaaca tttttggate acaetattte gaceeggaga
                                                                                  540
       35 actgcaggtt ccaacaccag acgctggaaa acgggtacga cgtctaccac tctcctcagt
       37 atcacttect ggteagtetg ggeegggega agagageett cetgeeagge atgaaceeae
       39 coccytacto coayttooty toccyyagga acyayatcoc cotaattoac ttoaacacco
                                                                                  660
                                                                                  720
       41 ccataccacg geggeacace eggagegeeg aggaegacte ggagegggae eeeetgaaeg
       43 tgctgaagee eegggeeegg atgaceeegg eeeeggeete etgtteaeag gageteeega
                                                                                  780
                                                                                  840
       45 gegeegagga caacageeeg atggeeagtg acceattagg ggtggteagg ggeggtegag
       47 tgaacacgca cgctggggga acgggcccgg aaggctgccg ccccttcgcc aagttcatct
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                                                                                  960
       49 agggtcgctg gaagggcacc ctctttaacc catccctcag caaacgcagc tcttcccaag
                                                                                 1020
       51 gaccaggtec citgacgtte egaggatggg aaaggtgaca ggggcatgta tggaattige
       53 tgcttctctg gggtcccttc cacaggaggt cctgtgagaa ccaacctttg aggcccaagt
      55 catggggttt caccgccttc ctcactccat atagaacacc tttcccaata ggaaacccca
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       57 acaggtaaac tagaaatttc cccttcatga aggtagagag aaggggtctc tcccaacata
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      59 tttctcttcc ttgtgcctct cctctttatc acttttaagc ataaaaaaaa aaaaaaaaa
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       61 aaaaaaaaaa aaaagcagtg ggttcctgag ctcaagactt tgaaggtgta gggaagagga
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       63 aatoggagat occagaaget totocactgo octatgoatt tatgttagat gooccgatoo
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                                                                                1440
       65 cactggcatt tgagtgtgca aaccttgaca ttaacagctg aatggggcaa gttgatgaaa
       67 acactactit caageetteg ticticettg ageatetetg gggaagaget gicaaaagae
                                                                                 1500
                                                                                1560
       69 tggtggtagg ctggtgaaaa cttgacagct agacttgatg cttgctgaaa tgaggcagga
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      74 <210> SEQ ID NO: 2
      75 <211> LENGTH: 251
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76 <212> TYPE: PRT

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Input Set : A:\PTO.YF.txt

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79 <400> SEQUENCE: 2
81 Met Leu Gly Ala Arg Leu Arg Leu Trp Val Cys Ala Leu Cys Ser Val
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84 Cys Ser Met Ser Val Leu Arg Ala Tyr Pro Asn Ala Ser Pro Leu Leu
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                                   25
87 Gly Ser Ser Trp Gly Gly Leu Ile His Leu Tyr Thr Ala Thr Ala Arg
                               40
90 Asn Ser Tyr His Leu Gln Ile His Lys Asn Gly His Val Asp Gly Ala
93 Pro His Gln Thr Ile Tyr Ser Ala Leu Met Ile Arg Ser Glu Asp Ala
                       70
                                            75
96 Gly Phe Val Val Ile Thr Gly Val Met Ser Arg Arg Tyr Leu Cys Met
                                        90
99 Asp Phe Arg Gly Asn Ile Phe Gly Ser His Tyr Phe Asp Pro Glu Asn
                100
                                    105
                                                         110
102 Cys Arg Phe Gln His Gln Thr Leu Glu Asn Gly Tyr Asp Val Tyr His
            115
                                120
105 Ser Pro Gln Tyr His Phe Leu Val Ser Leu Gly Arg Ala Lys Arg Ala
        130
                            135
                                                 140
108 Phe Leu Pro Gly Met Asn Pro Pro Pro Tyr Ser Gln Phe Leu Ser Arg
109 145
                        150
                                            155
111 Arg Asn Glu Ile Pro Leu Ile His Phe Asn Thr Pro Ile Pro Arg Arg
                                        170
                    165
                                                             175
114 His Thr Arg Ser Ala Glu Asp Asp Ser Glu Arg Asp Pro Leu Asn Val
                180
                                    185
117 Leu Lys Pro Arg Ala Arg Met Thr Pro Ala Pro Ala Ser Cys Ser Gln
            195
                                200
120 Glu Leu Pro Ser Ala Glu Asp Asn Ser Pro Met Ala Ser Asp Pro Leu
        210
                            215
                                                 220
123 Gly Val Val Arg Gly Gly Arg Val Asn Thr His Ala Gly Gly Thr Gly
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                                             235
126 Pro Glu Gly Cys Arg Pro Phe Ala Lys Phe Ile
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127
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130 <211> LENGTH: 1559
131 <212> TYPE: DNA
132 <213> ORGANISM: Mus sp.
134 <400> SEQUENCE: 3
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137 tagggacetg cettagacte etggtgggeg tgetetgeae tgtetgeage ttgggeaetg
                                                                          120
139 ctagageeta teeggaeaet teeceattge ttggeteeaa etggggaage etgaeeeaee
                                                                          180
141 tgtacacggc tacagccagg accagctate acctacagat ccatagggat ggtcatgtag
                                                                          240
143 atggcacccc ccatcagacc atctacagtg ccctgatgat tacatcagag gacgccggct
                                                                          300
145 ctgtggtgat aacaggagec atgactegaa ggtteetttg tatggatete caeggeaaca
                                                                          360
147 tttttggatc gcttcacttc agcccagaga attgcaagtt ccgccagtgg acgctggaga
                                                                          420
149 atggctatga cgtctacttg tcgcagaagc atcactacct ggtgagcctg ggccgcgcca
                                                                          480
151 agegeatett ceageeggge aceaaceege egecettete eeagtteetg getegeagga
                                                                          540
153 acgaggteec getgetgeat ttetacaetg ttegeceaeg gegeeaeaeg egeagegeeg
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155 aggacceace ggageggae ceaetgaaeg tgeteaagee geggeeege geeaegeetg
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157 tgcctgtatc ctgctctcgc gagctgccga gcgcagagga aggtggcccc gcagccagcg
                                                                          720
159 atcctctggg ggtgctgcgc agaggccgtg gagatgctcg cgggggcgcg ggaggcgcgg
                                                                          780
161 ataggtgtcg cccctttccc aggttcgtct aggtccccag gccaggctgc gtccgcctcc
                                                                          840
163 atcctccagt cggttcagcc cacgtagagg aaggactagg gtacctcgag gatgtctgct
                                                                          900
165 tetetecett eestatggge etgagagtea eetgegaggt teeageeagg caeegetatt
                                                                          960
167 cagaattaag agccaacggt gggaggctgg agaggtggcg cagacagttc tcagcaccca
                                                                         1020
169 caaatacctg taattotago tocaggggaa totgtactoa cacacacaca catocacaca
                                                                         1080
171 cacacacaca cacatacatg taattttaaa tqttaatctg atttaaagac cccaacaggt
173 aaactagaca cgaagctctt tttattttat tttactaaca ggtaaaccag acacttggcc
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175 tttattagcc gggtctcttg cctagcattt taatcgatca gttagcacga ggaaagagtt
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177 cacgcettga acacagggaa gaggecatet etgeagette tagttaetat tetgggatte
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179 acgggtgttt gagtttgagc accttgacct taatgtcttc actaggcaag tcgaagaaag
                                                                         1380
181 acgcgcattt cttctctttg ggaagagett tggattggcg ggaggetgac aaggacacet
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183 aaaccgaaca catttcagag ttcagcctcc ctgaggaatg attcgccaat gattctgtga
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189 <211> LENGTH: 251
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                                    25
201 Gly Ser Asn Trp Gly Ser Leu Thr His Leu Tyr Thr Ala Thr Ala Arg
204 Thr Ser Tyr His Leu Gln Ile His Arg Asp Gly His Val Asp Gly Thr
                            55
207 Pro His Gln Thr Ile Tyr Ser Ala Leu Met Ile Thr Ser Glu Asp Ala
208 65
                        70
210 Gly Ser Val Val Ile Thr Gly Ala Met Thr Arg Arg Phe Leu Cys Met
211
                    85
                                        90
213 Asp Leu His Gly Asn Ile Phe Gly Ser Leu His Phe Ser Pro Glu Asn
                100
                                    105
216 Cys Lys Phe Arg Gln Trp Thr Leu Glu Asn Gly Tyr Asp Val Tyr Leu
           115
                                120
219 Ser Gln Lys His His Tyr Leu Val Ser Leu Gly Arg Ala Lys Arg Ile
        130
                            135
                                                140
222 Phe Gln Pro Gly Thr Asn Pro Pro Phe Ser Gln Phe Leu Ala Arq
223 145
                        150
                                            155
225 Arg Asn Glu Val Pro Leu Leu His Phe Tyr Thr Val Arg Pro Arg Arg
                    165
                                        170
                                                             175
228 His Thr Arg Ser Ala Glu Asp Pro Pro Glu Arg Asp Pro Leu Asn Val
                                    185
231 Leu Lys Pro Arg Pro Arg Ala Thr Pro Val Pro Val Ser Cys Ser Arg
                                200
                                                     205
234 Glu Leu Pro Ser Ala Glu Glu Gly Gly Pro Ala Aia Ser Asp Pro Leu
235
        210
                            215
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/901,938A

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Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\11032003\I901938A.raw

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	Ala Asp Arg Cys Arg Pro Phe Pro Arg Phe Val	
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253	Asp	
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	<211> LENGTH: 25	
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	<211> LENGTH: 21	
	<212> TYPE: DNA	
	<213> ORGANISM: Homo sapiens <400> SEQUENCE: 10	
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	<211> LENGTH: 21	
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	<400> SEQUENCE: 11	
	teggegetee aggtgtgeeg e	21
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RAW SEQUENCE LISTING DATE: 11/04/2003 PATENT APPLICATION: Us/09/901,938A TIME: 10:01:50

Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\11032003\I901938A.raw

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312 <212> TYPE: DNA
313 <213> ORGANISM: Homo sapiens
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320 <211> LENGTH: 21
321 <212> TYPE: DNA
322 <213> ORGANISM: Homo sapiens
324 <400> SEQUENCE: 13
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328 <210> SEQ ID NO: 14
329 <211> LENGTH: 139
330 <212> TYPE: PRT
331 <213> ORGANISM: Homo Sapiens
333 <400> SEQUENCE: 14
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338 Gln Met His Pro Asp Gly Thr Ile Asp Gly Thr Lys Asp Glu Asn Ser
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341 Asp Tyr Thr Leu Phe Asn Leu Ile Pro Val Gly Leu Arg Val Val Ala
                                40
344 Ile Gln Gly Val Lys Ala Ser Leu Tyr Val Ala Met Asn Gly Glu Gly
                            55
347 Tyr Leu Tyr Ser Ser Asp Val Phe Thr Pro Glu Cys Lys Phe Lys Glu
                       70
                                           75
350 Ser Val Phe Glu Asn Tyr Tyr Val Ile Tyr Ser Ser Thr Leu Tyr Arg
                                        90
353 Gln Gln Glu Ser Gly Arg Ala Trp Phe Leu Gly Leu Asn Lys Glu Gly
               100
                                    105
356 Gln Ile Met Lys Gly Asn Arg Val Lys Lys Thr Lys Pro Ser Ser His
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359 Phe Val Pro Lys Pro Ile Glu Val Cys Met Tyr
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363 <211> LENGTH: 139
364 <212> TYPE: PRT
365 <213> ORGANISM: Homo Sapiens
367 <400> SEQUENCE: 15
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372 Gln Met His Pro Asp Gly Ala Leu Asp Gly Thr Lys Asp Asp Ser Thr
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375 Asn Ser Thr Leu Phe Asn Leu Ile Pro Val Gly Leu Arg Val Val Ala
                                40
378 Ile Gln Gly Val Lys Thr Gly Leu Tyr Ile Ala Mct Asn Gly Glu Gly
381 Tyr Leu Tyr Pro Ser Glu Leu Phe Thr Pro Glu Cys Lys Phe Lys Glu
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70

382 65

RAW SEQUENCE LISTING ERROR SUMMARY DATE PATENT APPLICATION: US/09/901,938A

DATE: 11/04/2003 TIME: 10:01:51

Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\11032003\I901938A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:35; Xaa Pos. 2,3,4

VERIFICATION SUMMARY

DATE: 11/04/2003 PATENT APPLICATION: US/09/901,938A TIME: 10:01:51

Input Set : A:\PTO.YF.txt

Output Set: N:\CRF4\11032003\I901938A.raw

L:4 M:283 W: Missing Blank Line separator, <120> field identifier L:5 M:283 W: Missing Blank Line separator, <140> field identifier L:0 M:201 W: Mandatory field data missing, <130> FILE REFERENCE L:6 M:271 C: Current Filing Date differs, Replaced Current Filing Date L:10 M:283 W: Missing Blank Line separator, <160> field identifier L:1061 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:35 L:1070 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:35 L:1079 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35 after pos.:0